

1/24

2/24	3/24
4/24	5/24
6/24	7/24

Fig. 1

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-60 tgaaaagatagaataaaatggcctcgtg

1 ATGGCGCGGCCAGCGCTGCTGGGCGAG
1 M A R P A L L G E

61 GGCCAAGTTGCCGCGGCCACAGAAGTT
21 G Q V A A A T E V

121 GAAAATCTCTGCACGATAATATGGACG
41 E N L C T I I W T

181 ACTCTCAGATATTTTAGTCACTTTGAT
61 T L R Y F S H F D

241 CATCGTAAAGAGGAATTACCCCTGGAT
81 H R K E E L P L D

301 AGTGCCAATGAAAGTGAGAAGCCTAGC
101 S A N E S E K P S

361 GGTGATCCTGAGTCCGCTGTGACTGAG
121 G D P E S A V T E

421 AAGTGTTTCCTGGCTCCCTGGAAGGAAT
141 K C S W L P G R N

Fig. 1(i)

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ccgaattcggcacgagccgagggcgaggggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG

L L V L L L W T A T V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT

E K I C L Q V G S Q C

CCTTTGGTGAAAAAGTGCATCTCACCCCCCTGAA

P L V K K C I S P P E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG

L K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

T S P D T H Y T L Y Y

Fig. 1(ii)

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481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTTCCTTTAAATTGACTAAA
181	I A C S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L W S D W S E

Fig. 1(iii)

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CAATGTGAAAACATCTATAGAGAAGGTCAACAC

Q C E N I Y R E G Q H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA

V E P S F E H Q N V Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT

I R P S C K I V S L T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA

I K H L L L K N G A L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG

F R S R C L T Y E V E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG

N I L E V E E D K C Q

GGTACAAGTTGTTTCCAACCTCCCTGGTGTCTT

G T S C F Q L P G V L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC

R V K T N K L C F D D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC

A Q S I G K E Q N S T

Fig. 1(iv)

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1021 TTCTACACCACCATGTTACTCACCATT
341 F Y T T M L L T I

1081 CTTTTTACCTGAAAAGGCTTAAGATC
361 L F Y L K R L K I

1141 ATTTTAAAGAAATGTTTGGAGACCAG
381 I F K E M F G D Q

1201 ATCTATGAGAAACAATCCAAAGAAGAA
401 I Y E K Q S K E E

1261 AAAGCAGCTCCTTGAtggggagaaagtg
421 K A A P *

1321 gatttattgcattctccatttgttatc
1381 cttgaaaaaacaggcagctcctaagagc
1441 ccaaacccaaaggagctccttccaaga
1501 ccctaaaagcagatgttttgccaaatc
1561 accatcaattcatctaatacaggaattg

Fig. 1(v)

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CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
P V F V A V A V I I L

ATTATATTTCTCCAATTCCTGATCCTGGCAAG
I I F P P I P D P G K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
N D D T L H W K K Y D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
T D S V V L I E N L K

atttcttttcttgccttcaatgtgaccctgtgaa

tgggggacttggttaaataagaaactgaaactact
cacaggtcttgatgtgacttttgcattgaaaac
aaagcaagagttcttctcgttccttggtccaat
cccaaactagaggacaaagacaaggggacaatg
tgatggcttcctaaggaatctctgcttgctctg

Fig. 1(vi)

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NR4 EXPRESSION IN MOUSE TISSUES

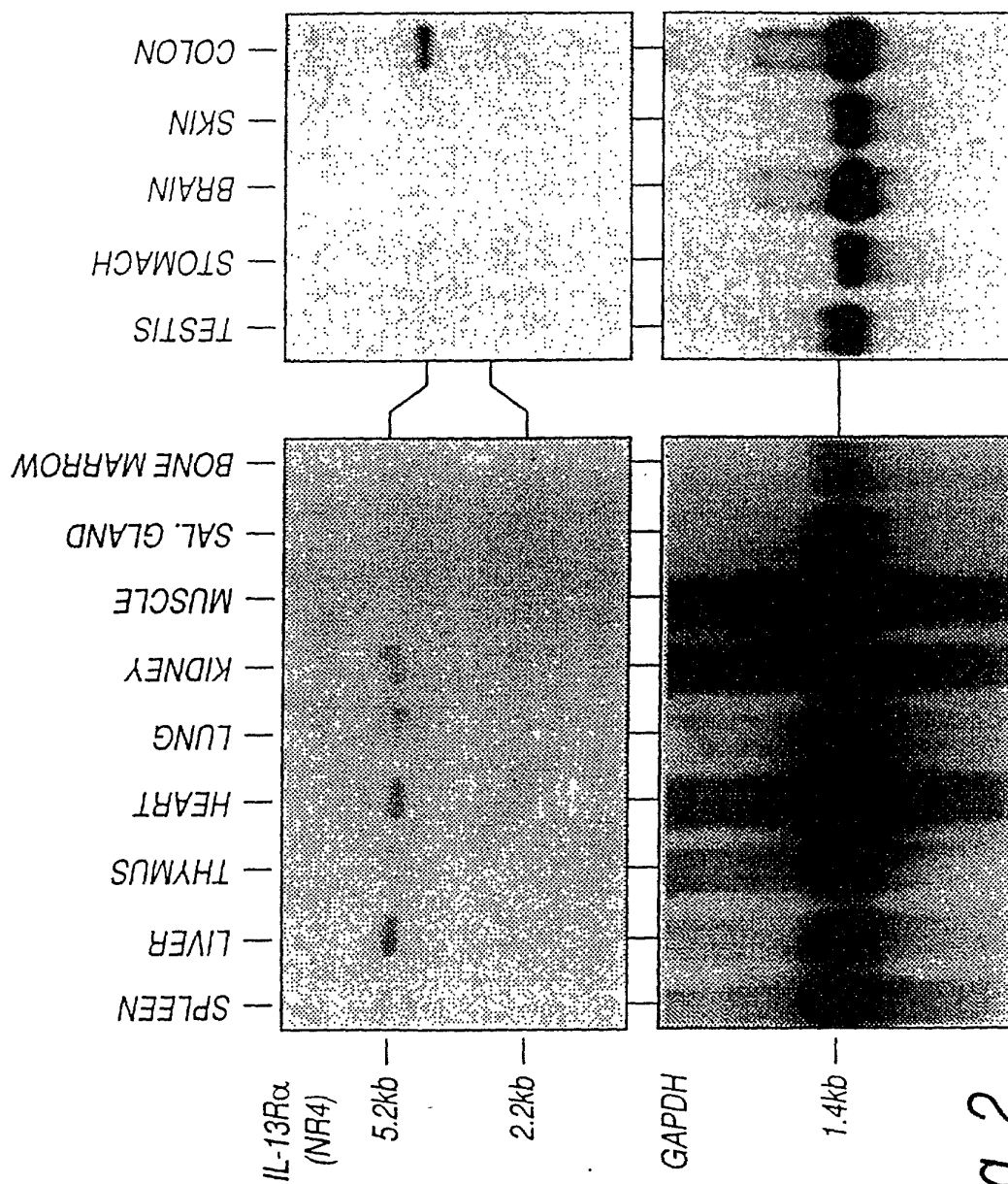


Fig. 2

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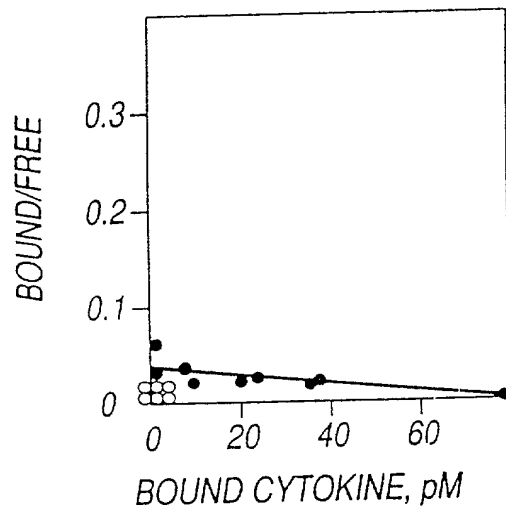


Fig. 3(A)

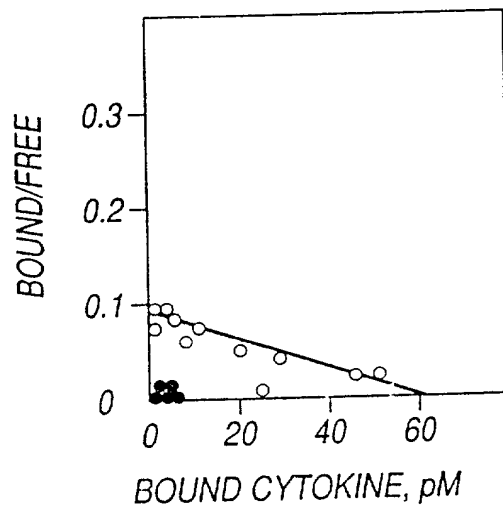


Fig. 3(B)

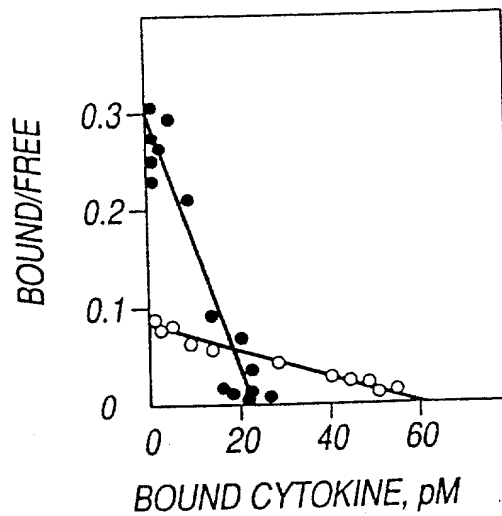
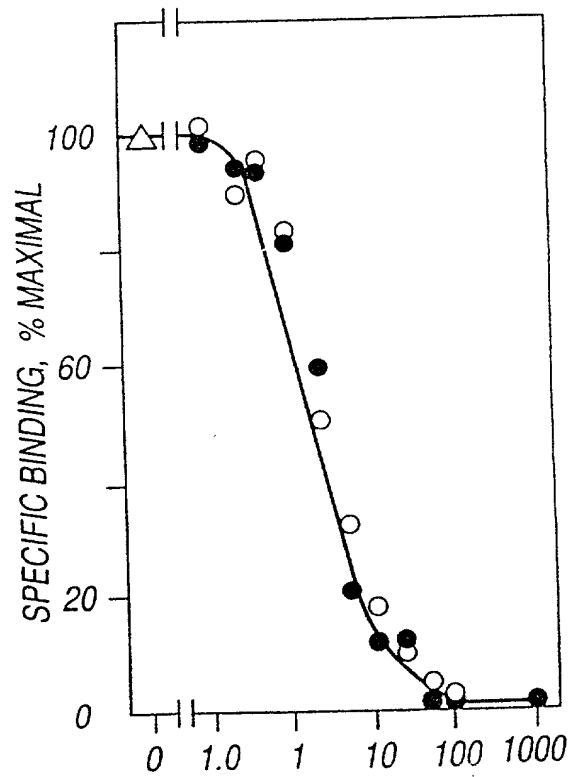
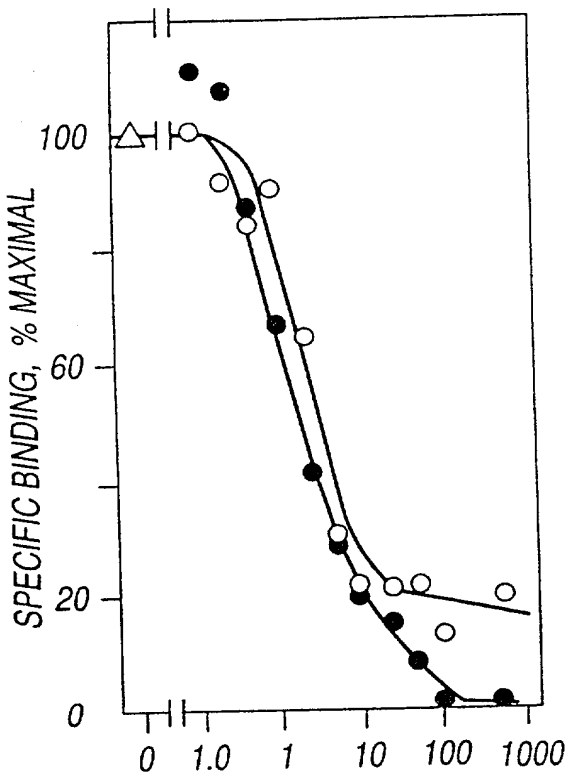
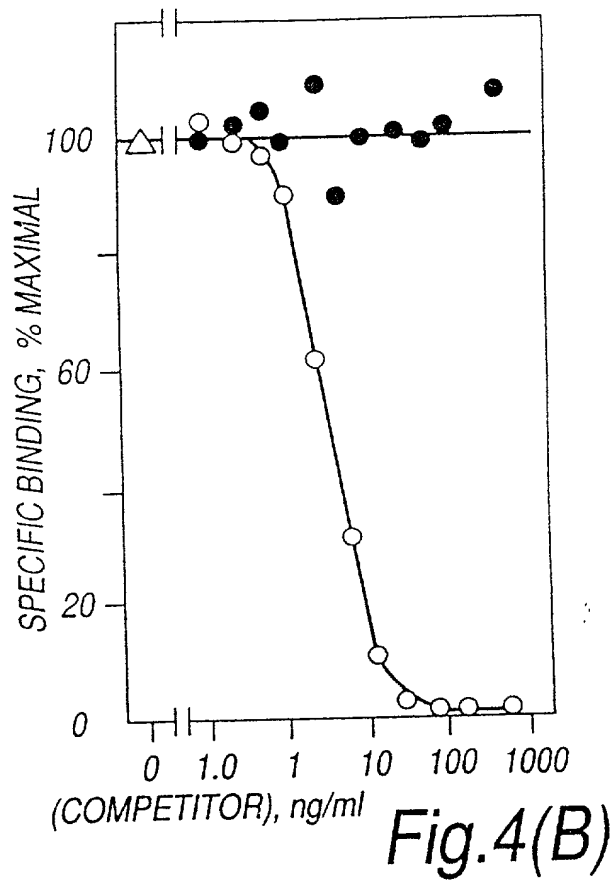
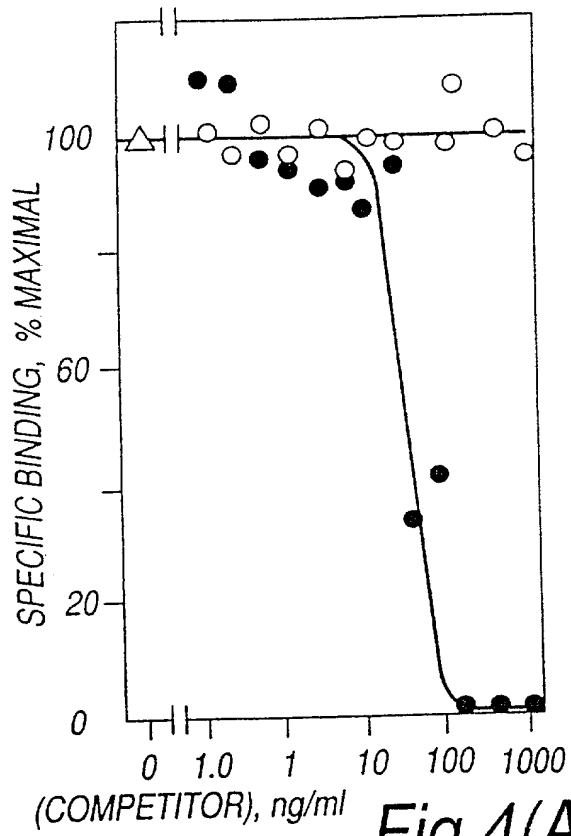


Fig. 3(C)

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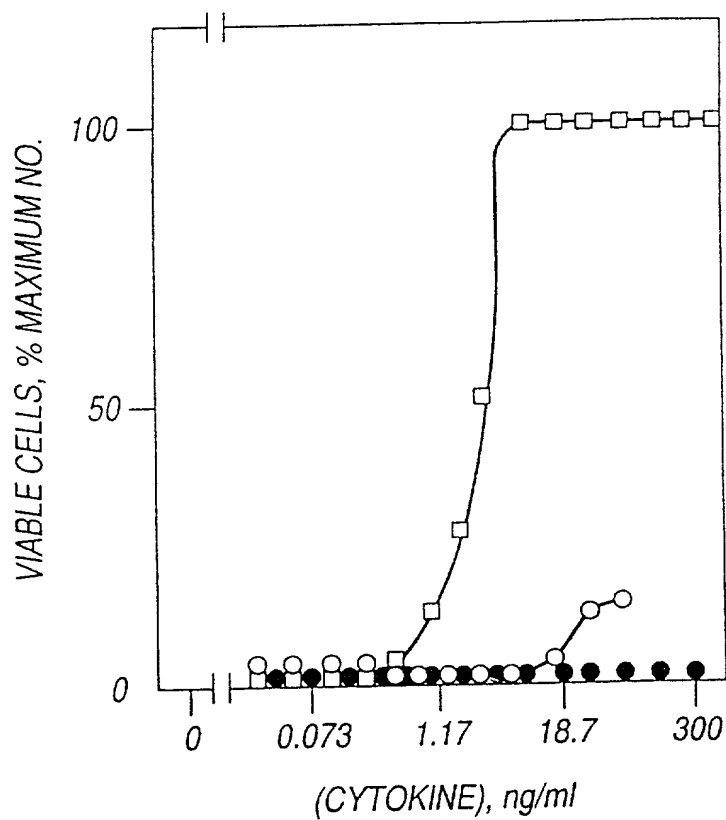
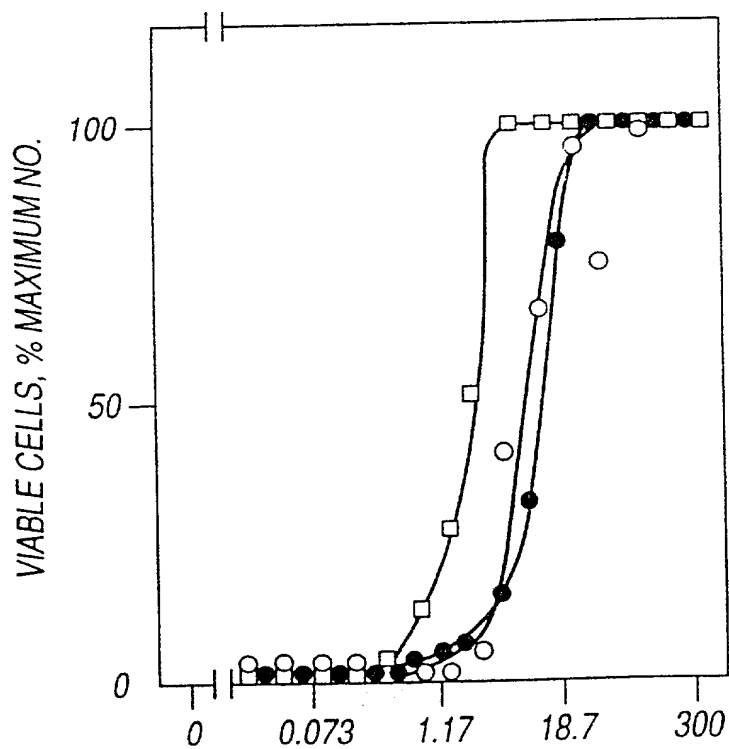


Fig. 5(A)



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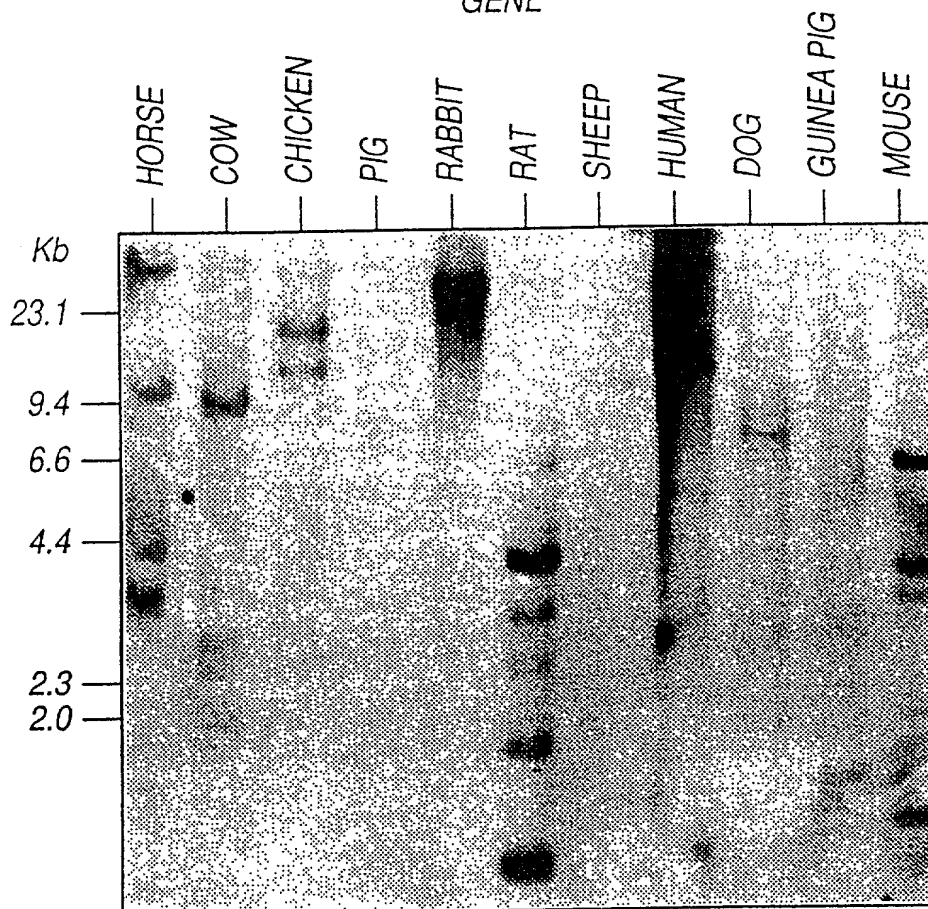
CROSS-SPECIES CONSERVATION OF THE NR-4 (IL-13R α)
GENE

Fig. 6

(major)

DYKDD	DDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

(minor)

ASISS	SDYKD	DDESR	TEVQP	PVTXL	SV
1	5	10	15	20	25

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14/24	15/24
16/24	17/24
18/24	19/24
20/24	21/24
22/24	23/24

Fig. 7

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H		gagtctaacacggaccaaggagtttaac
M	-60	tgaaaagatagaataaatggcctcgtgc
H		M E W P A R L C G
		ATGGAGTGGCCGGCGCGGCTCTGCGGGC
		* * * *
M	1	ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M	1	M A R P A L L G E
H		G G G G A P T E T
H		GGGGGCGGGGGCGCGCCTACGGAAACTC
		* * * *
M	61	GGCCAAGTTGCCGCGGCCACAGAAGTTC
M	21	G Q V A A A T E V
H		E N L C T V I W T
H		GAAAACCTCTGCACAGTAATATGGACAT
		* * * * * * *
M	121	GAAAATCTCTGCACGATAATATGGACGT
M	41	E N L C T I I W T
H		S L W Y F S H F G
H		AGTCTATGGTATTTTAGTCATTTTGGCG
		* * * * *
M	181	ACTCTCAGATATTTTAGTCACTTTGATG
M	61	T L R Y F S H F D

Fig. 7(i)

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acgtgcggccggggttccgagggcgagaggctgc

.....

cgaattcggcacgagccgagggcgagggcctgc

L W A L L L C A G G G G
 TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC

* * * *

TGTTGGTGCTGCTACTGTGGACCGCCACCGTG---

L L V L L L W T A T V -

Q P P V T N L S V S V
 AGCCACCTGTGACAAATTTGAGTGTCTCTGTT

* * * * *

AGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

W N P P E G A S S N C
 GGAATCCACCCGAGGGAGCCAGCTCAAATTGT

* * * * *

GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

D K Q D K K I A P E T
 ACAAACAAGATAAGAAAATAGCTCCGGAAACT

* * * * *

ACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

Fig. 7(ii)

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H		R	R	S	I	E	V	P	L	N
H		CGTCGTTCAATAGAAGTACCCCTGAATG								
		*		*		*		*		*
M	241	CATCGTAAAGAGGAATTACCCCTGGATG								
M	81	H	R	K	E	E	L	P	L	D
H		S	T	N	E	S	E	K	P	S
H		AGCACCAATGAGAGTGAGAAGCCTAGCA								
		*		*	*	*	*	*	*	*
M	301	AGTGCCAATGAAAGTGAGAAGCCTAGCC								
M	101	S	A	N	E	S	E	K	P	S
H		G	D	P	E	S	A	V	T	E
H		GGTGATCCTGAGTCTGCTGTGACTGAAC								
		*	*	*	*	*	*	*	*	*
M	361	GGTGATCCTGAGTCCGCTGTGACTGAGC								
M	121	G	D	P	E	S	A	V	T	E
H		K	C	S	W	L	P	G	R	N
H		AAGTGTTCTTGGCTCCCTGGAAGGAATA								
		*	*	*	*	*	*	*	*	*
M	421	AAGTGTTCTTGGCTCCCTGGAAGGAATA								
M	141	K	C	S	W	L	P	G	R	N
H		W	H	R	S	L	E	K	I	H
H		TGGCACAGAAGCCTGGAAAAAATTCATC								

Fig. 7(iii)

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E R I C L Q V G S Q C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
* * * * *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C

I L V E K C I S P P E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
* * * * *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P L V K K C I S P P E

L Q C I W H N L S Y M
TTCAATGCATTTGGCACAACCTGAGCTACATG
* * * * *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M

T S P D T N Y T L Y Y
CCAGTCCCGACACTAACTATACTCTCTACTAT
* * * * *
CAAGCCCTGACACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Q C E N I F R E G Q Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC

Fig. 7(iv)

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		* *
M	481	TGGTACAGCAGCCTGGAGAAAAGTCGTC
M	161	W Y S S L E K S R
H		F G C S F D L T K
H		TTTGGTTGTTCCTTTGATCTGACCAAAG
		* *
M	541	ATTGCTTGTTTCCTTTAAATTGACTAAAG
M	181	I A C S F K L T K
H		Q I M V K D N A G
H		CAAATAATGGTCAAGGATAATGCAGGAA
		* *
M	601	CAAATAATGGTCAAGGATAATGCTGGGA
M	201	Q I M V K D N A G
H		T S R V K P D P P
H		ACTTCCCGTGTGAAACCTGATCCTCCAC
		* *
M	661	ACTTCCTATGTGAAACCTGATCCTCCAC
M	221	T S Y V K P D P P
H		L Y V Q W E N P Q
H		CTATATGTGCAATGGGAGAATCCACAGA
		* *
M	721	TTATTAGTGCAGTGGAAGAATCCACAAA
M	241	L L V Q W K N P Q

Fig. 7(v)

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```

*   *   *   *   *       *   *   *   *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q   C   E   N   I   Y   R   E   G   Q   H

V   K   D   S   S   F   E   Q   H   S   V
TGAAGGATTCCAGTTTGAACAACACAGTGTC
*               *   *   *               *
TGGAACCT- - -AGTTTGAACATCAGAACG TT
V   E   P   -   S   F   E   H   Q   N   V

K   I   K   P   S   F   N   I   V   P   L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
*   *           *   *           *   *   *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K   I   R   P   S   C   K   I   V   S   L

H   I   K   N   L   S   F   H   N   D   D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
*   *   *           *               *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H   I   K   H   L   L   L   K   N   G   A

N   F   I   S   R   C   L   F   Y   E   V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
*   *           *   *   *   *           *   *   *
ATTTTAGAAGCAGATGCTTAACCTTATGAAGTG
N   F   R   S   R   C   L   T   Y   E   V

```

Fig. 7(vi)

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H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*		*	*		
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
		*		*			*	*		
M	841	CAGAATTCCGAATCTGATAGAAACATGG								
M	281	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	901	CTTGCCGACGCTGTCTACACAGTCAGAG								
M	301	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*		*	*
M	961	GACAACAAACTGTGGAGTGATTGGAGTG								
M	321	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I
H		ACACTCTACATAACCATGTTACTCATTG								

Fig. 7(vii)

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H N V F Y V Q E A K C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
* * * * *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H N I L E V E E D K C

E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
* * * * *
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
E G T S C F Q L P G V

I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
* * * * *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D

Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
* * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S

V P V I V A G A I I V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

Fig. 7(viii)

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```

      *      *      *      *      *      *
M  1021 ACCTTCTACACCACCATGTTACTCACCA
M  341   T   F   Y   T   T   M   L   L   T

H      L   L   L   Y   L   K   R   L   K
H      CTCCTGCTTTACCTAAAAAGGCTCAAGA
      *   *           *   *   *   *   *   *
M  1081 CTCCTTTTTTACCTGAAAAGGCTTAAGA
M  361   L   L   F   Y   L   K   R   L   K

H      K   I   F   K   E   M   F   G   D
H      AAGATTTTAAAGAAATGTTTGGAGACC
      *   *   *   *   *   *   *   *   *
M  1141 AAGATTTTAAAGAAATGTTTGGAGACC
M  381   K   I   F   K   E   M   F   G   D

H      D   I   Y   E   K   Q   T   K   E
H      GACATCTATGAGAAGCAAACCAAGGAGG
      *   *   *   *   *   *           *   *
M  1201 GACATCTATGAGAAACAATCCAAAGAAG
M  401   D   I   Y   E   K   Q   S   K   E

H      K   K   A   S   Q   *
H      AAGAAAGCCTCTCAGTGAtggagataat
      *   *   *

M  1261 AAGAAAGCAGCTCCTTGAtgggggagaag
M  421   K   K   A   A   P   *

```

Fig. 7(ix)

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* * * * *

TTCCAGTCTTTGTCGCGAGTGGCAGTCATAATC

I P V F V A V A V I I

I I I F P P I P D P G

TTATTATATTCCCTCCAATTCCTGATCCTGGC

* * * * *

TCATTATATTTCTCCAATTCCTGATCCTGGC

I I I F P P I P D P G

Q N D D T L H W K K Y

AGAATGATGATACTCTGCACTGGAAGAAGTAC

* * * * *

AGAATGATGATACCCTGCACTGGAAGAAGTAT

Q N D D T L H W K K Y

E T D S V V L I E N L

AAACCGACTCTGTAGTGCTGATAGAAAACCTG

* * * * *

AAACGGATTCTGTAGTGCTGATAGAAAACCTG

E T D S V V L I E N L

ttattttttaccttcactgtgaccttgagaaga

tgattttcttttcttgccttcaatgtgaccctgt

Fig. 7(x)

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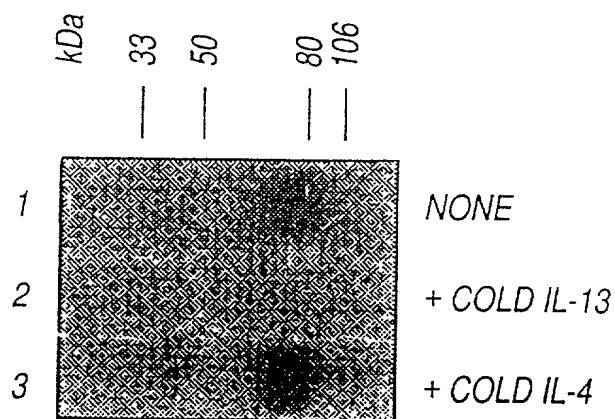


Fig. 8

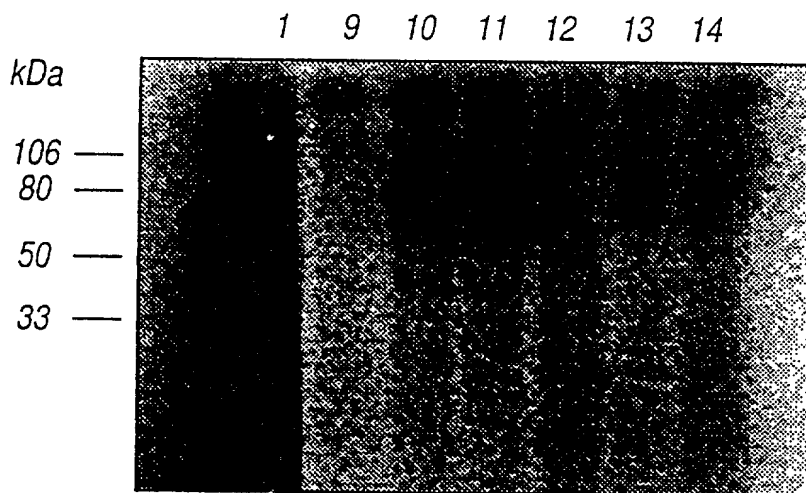


Fig. 9